

Currently Pending Claim Set

1. (Amended) A method for designing a zinc finger protein comprising a first (F1), a second (F2), and a third (F3) zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus that binds to a target site comprising, in 3' to 5' direction, a first (S1), a second (S2), and a third (S3) target subsite, each target subsite having the nucleotide sequence GNN, the method comprising the steps of

selecting the F1 zinc finger such that it binds to the S1 target subsite, wherein if S1 comprises GAA, F1 comprises the amino acid sequence QRSNLVR (SEQ ID NO:158); if S1 comprises GAG, F1 comprises the amino acid sequence RSDNLAR (SEQ ID NO:130); if S1 comprises GAC, F1 comprises the amino acid sequence DRSNLTR (SEQ ID NO:395); if S1 comprises GAT, F1 comprises the amino acid sequence QSSNLAR (SEQ ID NO:1765); if S1 comprises GGA, F1 comprises the amino acid sequence QSGHLAR (SEQ ID NO:413); if S1 comprises GGG, F1 comprises the amino acid sequence RSDHLAR (SEQ ID NO:127); if S1 comprises GGC, F1 comprises the amino acid sequence DRSHLTR (SEQ ID NO:1506); if S1 comprises GGT, F1 comprises the amino acid sequence QSSHLTR (SEQ ID NO:835); if S1 comprises GCA, F1 comprises QSGSLTR (SEQ ID NO:342); if S1 comprises GCG, F1 comprises RSDDLTR (SEQ ID NO:188); if S1 comprises GCC, F1 comprises ERGTLAR (SEQ ID NO:131); if S1 comprises GCT, F1 comprises the amino acid sequence QSSDLTR (SEQ ID NO:1450); if S1 comprises GTA, F1 comprises the amino acid sequence QSGALTR (SEQ ID NO:1398); if S1 comprises GTG, F1 comprises the amino acid sequence RSDALTR (SEQ ID NO:153); if S1 comprises GTC, F1 comprises the amino acid sequence DRSALAR (SEQ ID NO:184);

selecting the F2 zinc finger such that it binds to the S2 target subsite, wherein S2 comprises GAA, F2 comprises the amino acid sequence QSGNLAR (SEQ ID NO:801); if S2 comprises GAG, F2 comprises the amino acid sequence RSDNLAR (SEQ ID NO:130); if S2 comprises GAC, F2 comprises the amino acid sequence DRSNLTR (SEQ ID NO:395); if S2 comprises GAT, F2 comprises the amino acid sequence TSGNLVR (SEQ ID NO:1442); if S2 comprises GGA, F2

comprises the amino acid sequence QSGHLQR (SEQ ID NO:287); if S2 comprises GGG, F2 comprises the amino acid sequence RSDHLR (SEQ ID NO:229); if S2 comprises GGC, F2 comprises the amino acid sequence DRSHLAR (SEQ ID NO:1092); if S2 comprises GGT, F2 comprises the amino acid sequence TSGHLR (SEQ ID NO:1201); if S2 comprises GCA, F2 comprises the amino acid sequence QSGDLTR (SEQ ID NO:220); if S2 comprises GCG, F2 comprises the amino acid sequence RSDDLQR (SEQ ID NO:1844); if S2 comprises GCC, F2 comprises the amino acid sequence DRSDLTR (SEQ ID NO:417); if S2 comprises GCT, F2 comprises the amino acid sequence QSSDLTR (SEQ ID NO:1450); if S2 comprises GTA, F2 comprises the amino acid sequence QSGALAR (SEQ ID NO:3339); if S2 comprises GTG, F2 comprises the amino acid sequence RSDALR (SEQ ID NO:237); if S2 comprises GTC, F2 comprises the amino acid sequence DRALAR (SEQ ID NO:184); and

selecting the F3 zinc finger such that it binds to the S3 target subsite, wherein if S3 comprises GAA, F3 comprises the amino acid sequence QSGNLAR (SEQ ID NO:801); if S3 comprises GAG, F3 comprises the amino acid sequence RSDNLTR (SEQ ID NO:231); if S3 comprises GAC, F3 comprises the amino acid sequence DRSNLTR (SEQ ID NO:395); if S3 comprises GAT, F3 comprises the amino acid sequence TSANLNR (SEQ ID NO:377); if S3 comprises GGA, F3 comprises the amino acid sequence QSGHLQR (SEQ ID NO:287); if S3 comprises GGG, F3 comprises RSDHLR (SEQ ID NO:229); if S3 comprises GGT, F3 comprises the amino acid sequence TSGHLVR (SEQ ID NO:1425); if S3 comprises GCA, F3 comprises the amino acid sequence QSGDLTR (SEQ ID NO:220); if S3 comprises GCG, F3 comprises the amino acid sequence RSDDLTR (SEQ ID NO:188); if S3 comprises GCC, F3 comprises the amino acid sequence DRSDLTR (SEQ ID NO:417); if S3 comprises GCT, F3 comprises the amino acid sequence QSSDLQR (SEQ ID NO:132); if S3 comprises GTG, F3 comprises RSDALTR (SEQ ID NO:153); and if S3 comprises GTC, F3 comprises the amino acid sequence DRALAR (SEQ ID NO:184);

thereby designing a zinc finger protein that binds to a target site.